

FIGURE 1A

51

GGACTATTAGAGTGTGGAAACCGAAATAGTTTTGATAAAACAAGAAGTGCCTTTCGTTTTTGTATTTGTGAGAGAATTCA CCTGATAATCTCACACCTTGAGCTTTATCAAAACTATTTTGTTCTTCACGGAAAGCAAAAACATAAACACTCTCTTAAGT Gly Leu Leu Giu Cys Gly Thr Arg Asn Ser Phe Asp Lys Thr Arg Ser Ala Phe Arg Phe Cys Ile Cys Glu Arg Ile Gln GCAACTGAGAAAGAAGCTGATAATGCAAGAAGAGTAAAAGATTTCGATACAATGAAAGCAAAAACTAAAGAGGCTTTTG CGTTGACTCTTTCTTCGACTATTACGTTCTCTCATTTTCTAAAGCTATGTTACTTTCGTTTTTGATTTCTCCGAAAAC Gln Leu Arg Lys Glu Ala Asp Asn Ala Arg Arg Val Lys Asp Phe Asp Thr Met Lys Ala Lys Thr Lys Glu Ala Phe AATTGAGTTTTGTTTTTGATAAGGATTTTTTGAGTGAAAATAGAATTCAATGGAATGATATTTCTCACAACAAAAAAGAC TTAACTCAAAACAAAACTATTCCTAAAAAACTCACTTTTATCTTAAGTTACCTTACTATAAAGAGTGTTGTTTTTTCTG Glu Leu Ser Phe Val Phe Asp Lys Asp Phe Leu Ser Glu Asn Arg IIe Gln Trp Asn Asp IIe Ser His Asn Lys Lys Asp TCTGCAAGTAAAAGAAAACAATGAAAGAAGCGGACACAATGGATGATATTTTTAAGAGGGCTAAAAAATAATAAATCTAC AGACGTTCATTTTCTTTTTGTTACTTTCTTCGCCTGTGTTACCTACTATAAAAATTCTCCGATTTTTTATTATTTAGATG Ser Ala Ser Lys Arg Lys Thr Met Lys Glu Ala Asp Thr Met Asp Asp IIe Phe Lys Arg Leu Lys Asn Asn Lys Ser Thr ATATGATCGTTATGCTGGATTCCTTTCTATTTGTTCGATTACAGGTTGCAGACCAGCAGAAGTTTTAAAGGGTATAGAGA TATACTAGCAATACGACCTAAGGAAAGATAAACAAGCTAATGTCCAACGTCTGGTCGTCTTCAAAATTTCCCATATCTCT Tyr Asp Arg Tyr Ala Gly Phe Leu Ser IIe Cys Ser IIe Thr Gly Cys Arg Pro Ala Glu Val Leu Lys Gly IIe Glu TAGTAAGAAACAGATATGAGGATGGTATATCTTTTAAAATACTTGGTGCAAAGGTTGGAAATGACAGAGGGCAAAGCGAA ATCATTCTTTGTCTATACTCCTACCATATAGAAAATTTTATGAACCACGTTTCCAACCTTTACTGTCTCCCGTTTCGCTT lle Val Arg Asn Arg Tyr Glu Asp Gly Ile Ser Phe Lys Ile Leu Gly Ala Lys Val Gly Asn Asp Arg Gly Gln Ser Glu AGAACATTACATTTTGATTTATCAAAATATCATGATAATGAGCAAATGAATTATATTTTTGTCGCAATTAAAAGATAATAA 1360 TCTTGTAATGTAAAACTAAATAGTTTTATAGTACTATTACTCGTTTACTTAATATAAAACAGCGTTAATTTTCTATTATT Arg Thr Leu His Phe Asp Leu Ser Lys Tyr His Asp Asn Glu Gln Met Asn Tyr Ile Leu Ser Gln Leu Lys Asp Asn Lys ATTTTTCTACAAACCAGATGGGAAGCTCTACAACAGCTTGAGGCAATACCTCTACATCCAACATAGAACGTTTTCACTGT TAAAAAGATGTTTGGTCTACCCTTCGAGATGTTGTCGAACTCCGTTATGGAGATGTAGGTTGTATCTTGCAAAAGTGACA Phe Phe Tyr Lys Pro Asp Gly Lys Leu Tyr Asn Ser Leu Arg Gln Tyr Leu Tyr Ile Gln His Arg Thr Phe Ser Leu .ATACACTTCGTCACAGGGTTGCGAGTGATCTCAAGGCATCCGGTGCAGATGACTTCACCATAGCGGCTNTTTTGGGTCAC TATGTGAAGCAGTGTCCCAACGCTCACTAGAGTTCCGTAGGCCACGTCTACTGAAGTGGTATCGCCGANAAAACCCAGTG Tyr Thr Leu Arg His Arg Val Ala Ser Asp Leu Lys Ala Ser Gly Ala Asp Asp Phe Thr Ile Ala Ala ??? Leu Gly His

FIGURE 1B

Arg Val Thr Gin Ser Gin Giu Leu Leu Arg Leu Cys Ser Phe Val ??? Arg Trp Tyr Arg Cys Asn Trp Cys

AGATCTCAACCAGTTTAAAATCGCACTTCAAGAAGTAAAAATAGGGGCCGGCACCGGCTCTTTTTTTGGTGTTTTTTGTAG		
TCTAGAGTTGGTCAAATTTTAGCGTGAAGTTCTTCATTTTTATCCCCGGCCGTGGCCGAGAAAAAAAA		
TTAGTGGATATATCTGTTAGCTACAGAGAAAAGCGATTTTAGAGGGTTTGACGAGGTTTTTCGAGCTATCCAGGGTTTT		
AATCACCTATATAGACAATCGATGTCTCTTTTCGCTAAAATCTCCCAAAACTGCTCCAAAAAAGCTCGATAGGTCCCAAAA		
TGGGTTTTTGGGGTTGGATCAGAAAGTCGTTCAAGATTATTGACATAAAGACAGGAAGGTTTATAACAAGTACCAGATA	240	
ACCCAAAAACCCCAACCTAGTCTTTTCAGCAAGTTCTAATAACTGTATTTCTGTCCTTCCAAATATTGTTCATGGTCTAT		
CGACAAAACCAGCTTTGCAGGCTGGCTTTGAAGGACTAAAAGAAGTGGGGACTTCTTTGAGTCTTGTAATCAAGTTGGTC	220	
GCTGTTTTGGTCGAAACGTCCGACCGAAACTTCCTGATTTTCTTCACCCCTGAAGAAACTCAGAACATTAGTTCAACCAG		
AGAACTCGATTACGATTTGTAAGTAGAAATCTAACTCACATTTCGCAGAAAGTCAAACTTACCTCTTAGTTACAACTCAA	400	
TCTTGAGCTAATGCTAAACATTCATCTTTAGATTGAGTGTAAAGCGTCTTTCAGTTTGAATGGAGAATCAATGTTGAGTT		
AAATTTCCTAGCCTTTTCAGATCCTTAAGCATACATATTTTGTTTAAACCGATTGTGTCCGGTGTTTGGTGGAGCCAT	480	
TTTAAAGGATCGGAAAAGTCTAGGAATTCGTATGTATAAAACAAATTTGGCTAACACAGGCCACAAACCACACCTCGGTA		
TGATCCGAGTGGTCAATATGTGATTGTTCGCCAAACAGTGTATGTA	; - 560	
ACTAGGCTCACCAGTTATACACTAACAAGCGGTTTGTCACATACAT		
CGAAACGAGTGCCTAAGTGTTTTGGTTATCAACCAGGTAAGCTATGAGAAAGCCCAGCCATAAATGGGGTTAGGTTGAAG	- 640	
GCTTTGCTCACGGATTCACAAAACCAATAGTTGGTCCATTCGATACTCTTTCGGGTCGGTATTTACCCCAATCCAACTTC		
CAAGTCTTCATATGGTGCGACACAAGGGGTGTAGTAGGGTGTCGTCAAACTGAAAGGTTTGATAGCTCTAAGCTTGTGCT	720	
GTTCAGAAGTATACCACGCTGTGTTCCCCACATCATCCCACAGCAGTTTGACTTTCCAAACTATCGAGATTCGAACACGA		
TCTGTGGGTCAAGCCTCAAGTGCTGATCTGTGGTGTCGTCTACCTGATAACTTTCACTTTTTCGAGTGAAATTCAGGAGG	800	
AGACACCCAGTTCGGAGTTCACGACTAGACACCACAGCAGATGGACTATTGAAAAGTGAAAAAGCTCACTTTAAGTCCTCC		
CGAAACTATGGGTCAAGCCCAGCTTTGCTGGGGTTCGGCACATCCAGCTTACAGCATTGGTGCTCTTGCGAAGCTGAAGC	880	
GCTTTGATACCCAGTTCGGGTCGAAACGACCCCAAGCCGTGTAGGTCGAATGTCGTAACCACGAGAACGCTTCGACTTCG	000	

FIGURE 1D



FIGURE 1E

GAGATCT
CTCTAGA
1847

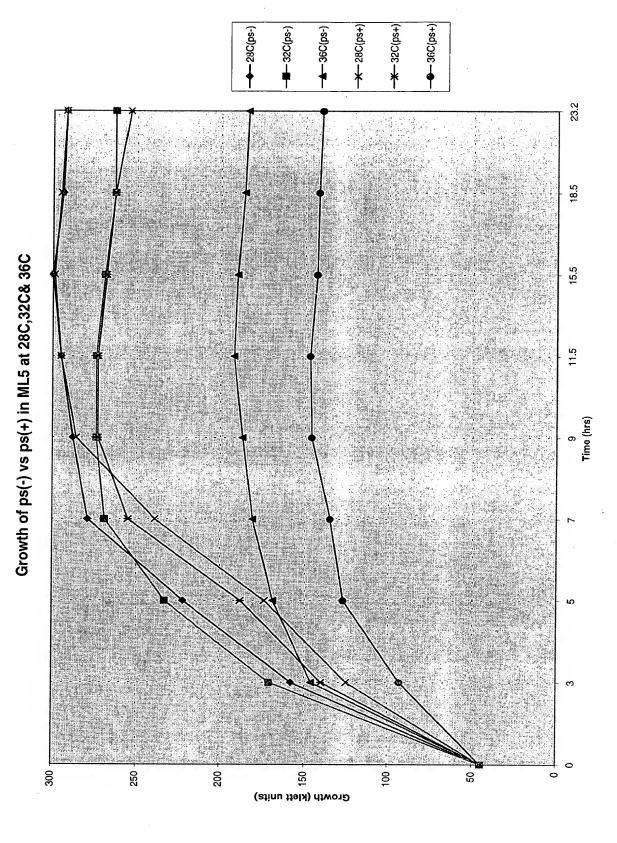


FIGURE 2

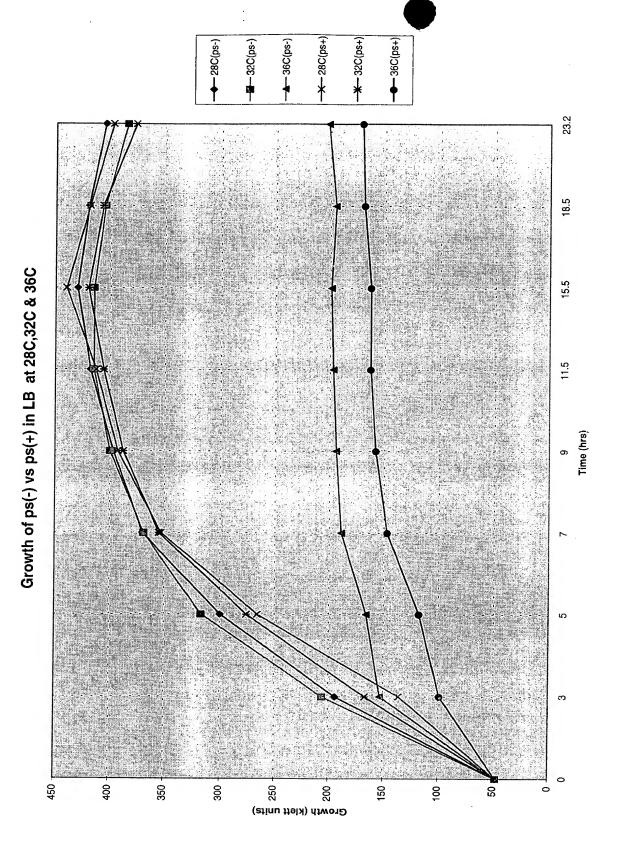


FIGURE 3